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0528

10

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RAW SEQUENCE LISTING

DATE: 06/03/2002

PATENT APPLICATION: US/09/940,921B

TIME: 13:52:47

Input Set : A:\LEX-0227-USA SEQLIST.txt

Output Set: N:\CRF3\06032002\I940921B.raw

4 <110> APPLICANT: Friddle, Carl Johan
5 Hilbun, Erin
6 Nepomnichy, Boris
7 Hu, Yi
9 <120> TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the
Same
11 <130> FILE REFERENCE: LEX-0227-USA
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/940,921B
C--> 13 <141> CURRENT FILING DATE: 2002-05-21
13 <150> PRIOR APPLICATION NUMBER: US 60/229,280
14 <151> PRIOR FILING DATE: 2000-08-31
16 <160> NUMBER OF SEQ ID NOS: 10
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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21 <211> LENGTH: 2052
22 <212> TYPE: DNA
23 <213> ORGANISM: homo sapiens
25 <400> SEQUENCE: 1
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27 gctaaaggga aatcagatag caagcactgt gtcataaaag agatcaattt tgaaaagatg 120
28 cccatacaag aaaaagaagc ttcaaagaaa gaagtgattc ttctggaaaa gatgaacat 180
29 cccaacattg tagccttctt caattcattt caagagaatg gcaggctgtt tattgtaatg 240
30 gaatattgtg atggagggga tctcatgaaa aggatcaata gacaacgggg tgtgttattt 300
31 agtgaagatc agatcctcgg ttggtttgta cagatttctc taggactaaa acatattcat 360
32 gacaggaaga tattacacag ggacataaaa gctcagaaca ttttcttag caagaacgga 420
33 atggtggcaa agcttgggga ctttggtata gcaagagtc tgaataattc catggaactt 480
34 gctogaactt gtattggaac accttactac ctgtccccag agatctgtca gaataaaccc 540
35 tacaacaata aaacggatat ttggtctctt ggctgtgtct tatatgagct ctgcacactt 600
36 aaacatcctt ttgagggtaa caacttacag cagctgggtc tgaagatttg tcaagcacat 660
37 tttgcccaca tatctccggg gtttctcgt gagctccatt ccttgatatc tcagctcttt 720
38 caagtatctc ctcgagaccg accatccata aattccattt tgaaaaggcc ctttttagag 780
39 aatcttattc ccaaatattt gactcctgag gtcattcagg aagaattcag tcacatgctt 840
40 atatgcagag caggagcgcc agcttctcga catgctggga aggtggtcca gaagtgtaaa 900
41 atacaaaaag tgagattcca gggaaagtgc ccaccaagat caaggatatc tgtgccaat 960
42 aaaaggaatg ctatattgca tagaaatgaa tggagaccac cagctggagc ccagaaggcc 1020
43 agatctataa aaatgataga aagacccaaa attgctgctg tctgtggaca ttatgattat 1080
44 tattatgctc aacttgatat gctgaggagg agagcccaca aaccaagtta tcaccctatt 1140
45 cctcaagaaa atactggagt tgaggattac ggtcaggaaa cgaggcatgg tccatcccca 1200
46 agtcaatggc ctgctgagta ccttcagaga aaatttgaag ctcaacaata taagttgaaa 1260
47 gtggagaagc aattgggtct tcgtccatct tctgccgagc caaattacaa ccagagacaa 1320
48 gagctaagaa gtaatggaga agagcctaga ttccaggagc tgccatttag gaaaaacgaa 1380
49 atgaaggaac aggaatattg gaagcagtta gaggaaatac gccaacagta ccacaatgac 1440
50 atgaaagaaa ttagaaagaa gatggggaga gaaccagagg agaactcaaa aataagtcac 1500
51 aaaacctatt tggatgaaga gagtaacctg cctgtccatc aagatgcac tgagggagaa 1560

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52 gcacctgtgc aggacattga aaaagacttg aaacaaatga ggcttcagaa cacaaaggaa 1620
53 agtaaaaatc cagaacagaa atataaagct aagaaggggg taaaatttga aattaattta 1680
54 gacaaatgta tttctgatga aaacatcctc caagaggaag aggcaatgga tataccaaat 1740
55 gaaactttga cctttgagga tggcatgaag tttaaggaat atgaatgtgt aaaggagcat 1800
56 ggagattata cagacaaagc atttgaaaaa cttcactgcc cagaagcagg gttttccacg 1860
57 cagactgtag ctgctgtggg aaacaggagg cagtgggatg gaggagcgcc tcagactctg 1920
58 ctgcagatga tggcagtggc cgacatcacc tccacctgcc ccacggggcc tgacagttag 1980
59 tctgtgctta gcgtcagtcg tcaggaaggg aagaccaagg acccgtagag cccagtgtc 2040
60 atcctgatgt ga 2052
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63 <211> LENGTH: 683
64 <212> TYPE: PRT
65 <213> ORGANISM: homo sapiens
67 <400> SEQUENCE: 2
68 Met Asp Lys Tyr Asp Val Ile Lys Ala Ile Gly Gln Gly Ala Phe Gly
69 1 5 10 15
70 Lys Ala Tyr Leu Ala Lys Gly Lys Ser Asp Ser Lys His Cys Val Ile
71 20 25 30
72 Lys Glu Ile Asn Phe Glu Lys Met Pro Ile Gln Glu Lys Glu Ala Ser
73 35 40 45
74 Lys Lys Glu Val Ile Leu Leu Glu Lys Met Lys His Pro Asn Ile Val
75 50 55 60
76 Ala Phe Phe Asn Ser Phe Gln Glu Asn Gly Arg Leu Phe Ile Val Met
77 65 70 75 80
78 Glu Tyr Cys Asp Gly Gly Asp Leu Met Lys Arg Ile Asn Arg Gln Arg
79 85 90 95
80 Gly Val Leu Phe Ser Glu Asp Gln Ile Leu Gly Trp Phe Val Gln Ile
81 100 105 110
82 Ser Leu Gly Leu Lys His Ile His Asp Arg Lys Ile Leu His Arg Asp
83 115 120 125
84 Ile Lys Ala Gln Asn Ile Phe Leu Ser Lys Asn Gly Met Val Ala Lys
85 130 135 140
86 Leu Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Asn Ser Met Glu Leu
87 145 150 155 160
88 Ala Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys
89 165 170 175
90 Gln Asn Lys Pro Tyr Asn Asn Lys Thr Asp Ile Trp Ser Leu Gly Cys
91 180 185 190
92 Val Leu Tyr Glu Leu Cys Thr Leu Lys His Pro Phe Glu Gly Asn Asn
93 195 200 205
94 Leu Gln Gln Leu Val Leu Lys Ile Cys Gln Ala His Phe Ala Pro Ile
95 210 215 220
96 Ser Pro Gly Phe Ser Arg Glu Leu His Ser Leu Ile Ser Gln Leu Phe
97 225 230 235 240
98 Gln Val Ser Pro Arg Asp Arg Pro Ser Ile Asn Ser Ile Leu Lys Arg
99 245 250 255
100 Pro Phe Leu Glu Asn Leu Ile Pro Lys Tyr Leu Thr Pro Glu Val Ile
101 260 265 270
102 Gln Glu Glu Phe Ser His Met Leu Ile Cys Arg Ala Gly Ala Pro Ala

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Input Set : A:\LEX-0227-USA SEQLIST.txt

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103          275          280          285
104 Ser Arg His Ala Gly Lys Val Val Gln Lys Cys Lys Ile Gln Lys Val
105          290          295          300
106 Arg Phe Gln Gly Lys Cys Pro Pro Arg Ser Arg Ile Ser Val Pro Ile
107 305          310          315          320
108 Lys Arg Asn Ala Ile Leu His Arg Asn Glu Trp Arg Pro Pro Ala Gly
109          325          330          335
110 Ala Gln Lys Ala Arg Ser Ile Lys Met Ile Glu Arg Pro Lys Ile Ala
111          340          345          350
112 Ala Val Cys Gly His Tyr Asp Tyr Tyr Tyr Ala Gln Leu Asp Met Leu
113          355          360          365
114 Arg Arg Arg Ala His Lys Pro Ser Tyr His Pro Ile Pro Gln Glu Asn
115          370          375          380
116 Thr Gly Val Glu Asp Tyr Gly Gln Glu Thr Arg His Gly Pro Ser Pro
117 385          390          395          400
118 Ser Gln Trp Pro Ala Glu Tyr Leu Gln Arg Lys Phe Glu Ala Gln Gln
119          405          410          415
120 Tyr Lys Leu Lys Val Glu Lys Gln Leu Gly Leu Arg Pro Ser Ser Ala
121          420          425          430
122 Glu Pro Asn Tyr Asn Gln Arg Gln Glu Leu Arg Ser Asn Gly Glu Glu
123          435          440          445
124 Pro Arg Phe Gln Glu Leu Pro Phe Arg Lys Asn Glu Met Lys Glu Gln
125          450          455          460
126 Glu Tyr Trp Lys Gln Leu Glu Glu Ile Arg Gln Gln Tyr His Asn Asp
127 465          470          475          480
128 Met Lys Glu Ile Arg Lys Lys Met Gly Arg Glu Pro Glu Glu Asn Ser
129          485          490          495
130 Lys Ile Ser His Lys Thr Tyr Leu Val Lys Lys Ser Asn Leu Pro Val
131          500          505          510
132 His Gln Asp Ala Ser Glu Gly Glu Ala Pro Val Gln Asp Ile Glu Lys
133          515          520          525
134 Asp Leu Lys Gln Met Arg Leu Gln Asn Thr Lys Glu Ser Lys Asn Pro
135          530          535          540
136 Glu Gln Lys Tyr Lys Ala Lys Lys Gly Val Lys Phe Glu Ile Asn Leu
137 545          550          555          560
138 Asp Lys Cys Ile Ser Asp Glu Asn Ile Leu Gln Glu Glu Glu Ala Met
139          565          570          575
140 Asp Ile Pro Asn Glu Thr Leu Thr Phe Glu Asp Gly Met Lys Phe Lys
141          580          585          590
142 Glu Tyr Glu Cys Val Lys Glu His Gly Asp Tyr Thr Asp Lys Ala Phe
143          595          600          605
144 Glu Lys Leu His Cys Pro Glu Ala Gly Phe Ser Thr Gln Thr Val Ala
145          610          615          620
146 Ala Val Gly Asn Arg Arg Gln Trp Asp Gly Gly Ala Pro Gln Thr Leu
147 625          630          635          640
148 Leu Gln Met Met Ala Val Ala Asp Ile Thr Ser Thr Cys Pro Thr Gly
149          645          650          655
150 Pro Asp Ser Glu Ser Val Leu Ser Val Ser Arg Gln Glu Gly Lys Thr
151          660          665          670

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152 Lys Asp Pro Tyr Ser Pro Val Leu Ile Leu Met
153          675                      680
155 <210> SEQ ID NO: 3
156 <211> LENGTH: 1965
157 <212> TYPE: DNA
158 <213> ORGANISM: homo sapiens
160 <400> SEQUENCE: 3
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162 gctaaaggga aatcagatag caagcactgt gtcataaaag agatcaattt tgaaaagatg      120
163 cccatacaag aaaaagaagc ttcaaagaaa gaagtgattc ttctggaaaa gatgaaacat      180
164 cccaacattg tagccttctt caattcattt caagagaatg gcaggctgtt tattgtaatg      240
165 gaatattgtg atggagggga tctcatgaaa aggatcaata gacaacgggg tgtgttattt      300
166 agtgaagatc agatcctcgg ttggtttgtg cagatttctc taggactaaa acatattcat      360
167 gacaggaaga tattacacag ggacataaaa gctcagaaca tttttcttag caagaacgga      420
168 atggtggcaa agcttgggga ctttgggtata gcaagagtcc tgaataattc catggaactt      480
169 gctcgaactt gtattggaac accttactac ctgtccccag agatctgtca gaataaaccc      540
170 tacaacaata aaacggatat ttggtctctt ggctgtgtct tatatgagct ctgcacactt      600
171 aaacatcctt ttgaggggtaa caacttacag cagctggttc tgaagatttg tcaagcacat      660
172 tttgccccaa tatctccggg gttttctcgt gagctccatt ccttgataac tcagctcttt      720
173 caagtatctc ctogagaccg accatccata aattccattt tgaaaaggcc ctttttagag      780
174 aatcttattc ccaaatattt gactcctgag gtcattcagg aagaattcag tcacatgctt      840
175 atatgcagag caggagcgcc agcttctcga catgctggga aggtggtcca gaagtgtaaa      900
176 atacaaaaag tgagattcca gggaaagtgc ccaccaagat caaggatatc tgtgccaatt      960
177 aaaaggaatg ctatattgca tagaaatgaa tggagaccac cagctggagc ccagaaggcc      1020
178 agatctataa aaatgataga aagacccaaa attgctgctg tctgtggaca ttatgattat      1080
179 tattatgctc aacttgatat gctgaggagg agagcccaca aaccaagtta tcaccctatt      1140
180 cctcaagaaa atactggagt tgaggattac ggtcaggaaa cgaggcatgg tccatcccca      1200
181 agtcaatggc ctgctgagta ccttcagaga aaatttgaag ctcaacaata taagttgaaa      1260
182 gtggagaagc aattgggtct tcgtccatct tctgccgagc caaattacaa ccagagacaa      1320
183 gagctaagaa gtaatggaga agagcctaga ttccaggagc tgccatttag gaaaaacgaa      1380
184 atgaaggaac aggagaactc aaaaataagt cataaaacct atttggtgaa gaagagtaac      1440
185 ctgcctgtcc atcaagatgc atctgagggg gaagcacctg tgcaggacat tgaaaaagac      1500
186 ttgaaacaaa tgaggcttca gaacacaaag gaaagtaaaa atccagaaca gaaatataaa      1560
187 gctaagaagg gggtaaaatt tgaaattaat ttagacaaat gtatttctga tgaaaacatc      1620
188 ctccaagagg aagaggcaat ggatatacca aatgaaactt tgacctttga ggatggcatg      1680
189 aagtttaagg aatatgaatg tgtaaaggag catggagatt atacagacaa agcatttgaa      1740
190 aaacttcaact gcccagaagc agggttttcc acgcagactg tagctgctgt gggaacaggy      1800
191 aggcagtggg atggaggagc gcctcagact ctgctgcaga tgatggcagt ggccgacatc      1860
192 acctccacct gcccacggg gcctgacagt gagtctgtgc ttagcgtcag tcgtcaggaa      1920
193 ggggaagacca aggaccgta cagcccagtg ctcatcctga tgtga      1965
195 <210> SEQ ID NO: 4
196 <211> LENGTH: 654
197 <212> TYPE: PRT
198 <213> ORGANISM: homo sapiens
200 <400> SEQUENCE: 4
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202 1          5                      10                      15
203 Lys Ala Tyr Leu Ala Lys Gly Lys Ser Asp Ser Lys His Cys Val Ile
204          20                      25                      30

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205 Lys Glu Ile Asn Phe Glu Lys Met Pro Ile Gln Glu Lys Glu Ala Ser
206          35          40          45
207 Lys Lys Glu Val Ile Leu Leu Glu Lys Met Lys His Pro Asn Ile Val
208          50          55          60
209 Ala Phe Phe Asn Ser Phe Gln Glu Asn Gly Arg Leu Phe Ile Val Met
210 65          70          75          80
211 Glu Tyr Cys Asp Gly Gly Asp Leu Met Lys Arg Ile Asn Arg Gln Arg
212          85          90          95
213 Gly Val Leu Phe Ser Glu Asp Gln Ile Leu Gly Trp Phe Val Gln Ile
214          100          105          110
215 Ser Leu Gly Leu Lys His Ile His Asp Arg Lys Ile Leu His Arg Asp
216          115          120          125
217 Ile Lys Ala Gln Asn Ile Phe Leu Ser Lys Asn Gly Met Val Ala Lys
218          130          135          140
219 Leu Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Asn Ser Met Glu Leu
220 145          150          155          160
221 Ala Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys
222          165          170          175
223 Gln Asn Lys Pro Tyr Asn Asn Lys Thr Asp Ile Trp Ser Leu Gly Cys
224          180          185          190
225 Val Leu Tyr Glu Leu Cys Thr Leu Lys His Pro Phe Glu Gly Asn Asn
226          195          200          205
227 Leu Gln Gln Leu Val Leu Lys Ile Cys Gln Ala His Phe Ala Pro Ile
228          210          215          220
229 Ser Pro Gly Phe Ser Arg Glu Leu His Ser Leu Ile Ser Gln Leu Phe
230 225          230          235          240
231 Gln Val Ser Pro Arg Asp Arg Pro Ser Ile Asn Ser Ile Leu Lys Arg
232          245          250          255
233 Pro Phe Leu Glu Asn Leu Ile Pro Lys Tyr Leu Thr Pro Glu Val Ile
234          260          265          270
235 Gln Glu Glu Phe Ser His Met Leu Ile Cys Arg Ala Gly Ala Pro Ala
236          275          280          285
237 Ser Arg His Ala Gly Lys Val Val Gln Lys Cys Lys Ile Gln Lys Val
238          290          295          300
239 Arg Phe Gln Gly Lys Cys Pro Pro Arg Ser Arg Ile Ser Val Pro Ile
240 305          310          315          320
241 Lys Arg Asn Ala Ile Leu His Arg Asn Glu Trp Arg Pro Pro Ala Gly
242          325          330          335
243 Ala Gln Lys Ala Arg Ser Ile Lys Met Ile Glu Arg Pro Lys Ile Ala
244          340          345          350
245 Ala Val Cys Gly His Tyr Asp Tyr Tyr Tyr Ala Gln Leu Asp Met Leu
246          355          360          365
247 Arg Arg Arg Ala His Lys Pro Ser Tyr His Pro Ile Pro Gln Glu Asn
248          370          375          380
249 Thr Gly Val Glu Asp Tyr Gly Gln Glu Thr Arg His Gly Pro Ser Pro
250 385          390          395          400
251 Ser Gln Trp Pro Ala Glu Tyr Leu Gln Arg Lys Phe Glu Ala Gln Gln
252          405          410          415
253 Tyr Lys Leu Lys Val Glu Lys Gln Leu Gly Leu Arg Pro Ser Ser Ala

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VERIFICATION SUMMARY

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PATENT APPLICATION: US/09/940,921B

TIME: 13:52:48

Input Set : A:\LEX-0227-USA SEQLIST.txt

Output Set: N:\CRF3\06032002\I940921B.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date